SEQUENCE LISTING

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Kraal, Barend
Luiten, Rudolf

<120> REDUCING BRANCHING AND ENHANCING FRAGMENTATION IN CULTURING FILAMENTOUS MICROORGANISMS

<130> 2183-4666US

<140> US 09/749,185
<141> 2000-12-26

<150> EP 98202148.7
<151> 1998-06-26

<160> 13

<170> PatentIn version 3.0

<210> 1
<211> 438
<212> DNA
<213> Streptomyces griseus

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ttccgtattc cggtggagct ccgatacgag gtcggcgatc cgtatgccat ccggatgacg 120

ttccaccttc ccggcgatgc ccctgtgacc tgggcgttcg gccgcgagct gctgctggac 180

gggctcaaca gcccgagcgg cgacggcgat gtgcacatcg gcccgaccga gcccgagggc 240

ctcggagatg tccacatccg gctccaggtc ggcgcggacc gtgcgctgtt ccgggcgggg 300

acggcaccgc tggtggcgtt cctcgaccgg acggacaagc tcgtgccgct cggccaggag 360

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<220>
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1 5 10 15

ctc cga tac gag gtc ggc gat ccg tat gcc atc cgg atg acg ttc cac
96
Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His

20 25 30

ctt ccc ggc gat gcc cct gtg acc tgg gcg ttc ggc cgc gag ctg ctg
144
Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu

35 40 45

ctg gac ggg ctc aac agc ccg agc ggc gac ggc gat gtg cac atc ggc
192
Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly

50 55 60

ccg acc gag ccc gag ggc ctc gga gat gtc cac atc cgg ctc cag gtc
240
Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val

65 70 75 80

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ggc gcg gac cgt gcg ctg ttc cgg gcg ggg acg gca ccg ctg gtg gcg
  288
Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala

                85                  90                  95


ttc ctc gac cgg acg gac aag ctc gtg ccg ctc ggc cag gag cac acg
  336
Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr

            100                 105                 110


ctg ggt gac ttc gac ggc aac ctg gag gac gca ctg ggc cgc atc ctc
  384
Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu

        115                 120                 125


gcc gag gag cag aac gcc ggc tg
  407
Ala Glu Glu Gln Asn Ala Gly

    130                 135
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<210> 3
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<213> Streptomyces griseus

<400> 3

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Leu Arg Tyr Glu Val Gly Asp Pro Tyr Ala Ile Arg Met Thr Phe His
            20                  25                  30


Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
        35                  40                  45
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Leu Asp Gly Leu Asn Ser Pro Ser Gly Asp Gly Asp Val His Ile Gly
50 55 60

Pro Thr Glu Pro Glu Gly Leu Gly Asp Val His Ile Arg Leu Gln Val
65 70 75 80

Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Thr Ala Pro Leu Val Ala
85 90 95

Phe Leu Asp Arg Thr Asp Lys Leu Val Pro Leu Gly Gln Glu His Thr
100 105 110

Leu Gly Asp Phe Asp Gly Asn Leu Glu Asp Ala Leu Gly Arg Ile Leu
115 120 125

Ala Glu Glu Gln Asn Ala Gly
130 135

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48
Met Ser Phe Leu Val Ser Glu Glu Leu Ala Phe Arg Ile Pro Val Glu
1 5 10 15

ctg cgg tac gag acc gtc gat ccg tac gcg gtg cgg ctg acg ttc cac
96
Leu Arg Tyr Glu Thr Val Asp Pro Tyr Ala Val Arg Leu Thr Phe His
20 25 30

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ctc ccc gga gac gcc ccg gtc acc tgg gtc ttc ggg cgt gaa ctg ctg
  144
Leu Pro Gly Asp Ala Pro Val Thr Trp Val Phe Gly Arg Glu Leu Leu

        35                  40                  45

gtc gag gga gtc ctg gac gcc gcg ggc gac ggc gac gtc cgg gtc tgc
  192
Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys

    50                  55                  60

ccg gtg ggg cag acg gcc acc agg gag gtg cac atc acc ctc cag gtc
  240
Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val

65                  70                  75                  80

ggc tcc gag cag gcg ctc ttc cgc gtc ggc aag gcg ccg ctg ctc gcc
  288
Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala

                85                  90                  95

ttc ctc gac cgc acc gac cag ggc ttg tcg ctc ggc agc gag cgg gca
  336
Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala

            100                 105                 110

cac gcc gac ttc gac agc cac ctc gac gac gct ctg aac cgc agc ctc
  384
His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu

        115                 120                 125

gcc gag gag cag agc gcc ggc tg
  407
Ala Glu Glu Gln Ser Ala Gly

    130                 135
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<210> 5
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20 25 30

Leu Pro Gly Asp Ala Pro Val Thr Trp Val Phe Gly Arg Glu Leu Leu
35 40 45

Val Glu Gly Val Leu Asp Ala Ala Gly Asp Gly Asp Val Arg Val Cys
50 55 60

Pro Val Gly Gln Thr Ala Thr Arg Glu Val His Ile Thr Leu Gln Val
65 70 75 80

Gly Ser Glu Gln Ala Leu Phe Arg Val Gly Lys Ala Pro Leu Leu Ala
85 90 95

Phe Leu Asp Arg Thr Asp Gln Gly Leu Ser Leu Gly Ser Glu Arg Ala
100 105 110

His Ala Asp Phe Asp Ser His Leu Asp Asp Ala Leu Asn Arg Ser Leu
115 120 125

Ala Glu Glu Gln Ser Ala Gly
130 135

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<212> DNA
<213> Streptomyces goldeniensis

<220>
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Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Arg Ile Pro Val Glu

1 5 10 15

ctg cgt tac gag acc tgt gat ccc tac gcc gtg cgg ctg acc ttt cat
96
Leu Arg Tyr Glu Thr Cys Asp Pro Tyr Ala Val Arg Leu Thr Phe His

20 25 30

ctg ccc gga gat gcc ccg gtg acc tgg gcg ttc ggg cgg gag ttg ctc
144
Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu

35 40 45

atc gac gga ggt ccg cgg ccg tgc ggg gac ggg gac gtc cac atc gcg
192
Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala

50 55 60

ccc gcc gac ccg gag acg ttc ggc gag gtc ctg atc cgc ctg cag gtg
240
Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val

65 70 75 80

ggg agc gac cag gcg atg ttc cgg gtc ggc acg gcg ccg ctg gtg gcc
288
Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala

85 90 95

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ttc ctg gac cgc acg gac aag atc gtg ccg ctg ggg cag gag cgt tcc
  336
Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser

            100                 105                 110


ctc gcc gac ttc gac gcc ctg ctc gac gag gcg ctg gac cgc atc ctg
  384
Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu

        115                 120                 125


gcc gag gag cag aac gcc ggc tg
  407
Ala Glu Glu Gln Asn Ala Gly

    130                 135
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<400> 7

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            20                  25                  30


Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
        35                  40                  45


Ile Asp Gly Gly Pro Arg Pro Cys Gly Asp Gly Asp Val His Ile Ala
    50                  55                  60


Pro Ala Asp Pro Glu Thr Phe Gly Glu Val Leu Ile Arg Leu Gln Val
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65 70 75 80

Gly Ser Asp Gln Ala Met Phe Arg Val Gly Thr Ala Pro Leu Val Ala
85 90 95

Phe Leu Asp Arg Thr Asp Lys Ile Val Pro Leu Gly Gln Glu Arg Ser
100 105 110

Leu Ala Asp Phe Asp Ala Leu Leu Asp Glu Ala Leu Asp Arg Ile Leu
115 120 125

Ala Glu Glu Gln Asn Ala Gly
130 135

<210> 8
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<221> CDS
<222> (1)..(405)

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Met Ser Phe Leu Val Ser Glu Glu Leu Ser Phe Lys Ile Pro Val Glu

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ctg cga tac gag acc cgg gat ccc tac gcg gtg cgg atg acc ttc cac
96
Leu Arg Tyr Glu Thr Arg Asp Pro Tyr Ala Val Arg Met Thr Phe His

20 25 30

ctc ccc gga gac gcg cct gtg acc tgg gcg ttc ggc cgg gag ctg ctg
144
Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu

35 40 45

ctc gac ggg atc aac cgc ccg agc ggc gac ggc gac gtc cac atc gcc
192
Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala

50 55 60

ccg acc gac ccc gag ggc ctg tcg gac gtc tcc atc cgg ctc cag gtg
240
Pro Thr Asp Pro Glu Gly Leu Ser Asp Val Ser Ile Arg Leu Gln Val

65 70 75 80

ggc gcg gac cgc gcc ctc ttc cgt gca ggc gcc ccg ccg ctg gtc gcc
288
Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala

85 90 95

ttc ctc gac cgc acg gac aag tcg gtg ccg ctc ggt cag gaa cag act
336
Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr

100 105 110

ctg ggt gac ttc gag gac agc ctg gag gcc gcg ctc ggc aag atc ctc
384
Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu

115 120 125

gcc gag gag cag aac gcc ggc tg
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Ala Glu Glu Gln Asn Ala Gly

130 135

<210> 9
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<213> Streptomyces netropsis

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            20                  25                  30

Leu Pro Gly Asp Ala Pro Val Thr Trp Ala Phe Gly Arg Glu Leu Leu
        35                  40                  45

Leu Asp Gly Ile Asn Arg Pro Ser Gly Asp Gly Asp Val His Ile Ala
    50                  55                  60

Pro Thr Asp Pro Glu Gly Leu Ser Asp Val Ser Ile Arg Leu Gln Val
65                  70                  75                  80

Gly Ala Asp Arg Ala Leu Phe Arg Ala Gly Ala Pro Pro Leu Val Ala
                85                  90                  95

Phe Leu Asp Arg Thr Asp Lys Ser Val Pro Leu Gly Gln Glu Gln Thr
            100                 105                 110

Leu Gly Asp Phe Glu Asp Ser Leu Glu Ala Ala Leu Gly Lys Ile Leu
        115                 120                 125

Ala Glu Glu Gln Asn Ala Gly
    130                 135
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<211> 34
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<213> Primer ssg1

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<211> 32
<212> DNA
<213> Primer ssg2

<400> 11
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32

<210> 12
<211> 32
<212> DNA
<213> Primer ssg3

<400> 12
gggaattcca tatgcgcgag tcggttcaag ca
32

<210> 13
<211> 25
<212> DNA
<213> Primer ssg4

<400> 13
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25